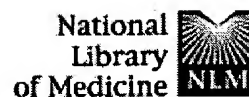


(FILE 'HOME' ENTERED AT 15:41:15 ON 17 AUG 2004)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 15:43:02 ON 17 AUG 2004

L1	651 S PYRROLIDINOL
L2	97 S L1 AND PYRROLIDINONE
L3	4 S L2 AND MICROCOCCUS
L4	4 DUP REM L3 (0 DUPLICATES REMOVED)
L5	6138 S MICROCOCCUS (2N) LUTEUS
L6	246 S L5 AND (REDUCTASE OR REDUCTION)
L7	24 S L5 (10N) (REDUCTASE OR REDUCTION)
L8	21 DUP REM L7 (3 DUPLICATES REMOVED)
L9	35 S L2 AND (REDUCTION OR ASYMETRICALLY)
L10	33 DUP REM L9 (2 DUPLICATES REMOVED)



Entrez PubMed Nucleotide Protein Genome Structure OMIM PMC Journals Br

Search PubMed for

☒ Limits Preview/Index History Clipboard Details

About Entrez

Text Version

Entrez PubMed

Overview

Help | FAQ

Tutorial

New/Noteworthy

E-Utilities

PubMed Services

Journals Database

MeSH Database

Single Citation Matcher

Batch Citation Matcher

Clinical Queries

LinkOut

Cubby

Related Resources

Order Documents

NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.
- Click on query # to add to strategy

Search	Most Recent Queries	Time	Result
#14	Search nadph pyrrolidinone Limits: Publication Date to 1999	11:25:08	62
#13	Search nadph carbonyl reductase micrococcus Limits: Publication Date to 1999	10:58:07	0
#11	Search nadph carbonyl reductase asymmetric Limits: Publication Date to 1999	10:57:15	1
#9	Search nadph carbonyl reductase pyrrolidinone Limits: Publication Date to 1999	10:56:50	0
#8	Search nadph carbonyl reductase Field: All Fields , Limits: Publication Date to 1999	10:56:32	135
#7	Search nadph carbonyl reductase Field: All Fields , Limits: Publication Date to 2000	10:56:17	147
#6	Search nadph carbonyl reductase	10:56:04	200
#5	Search micrococcus luteus nadph	10:55:40	7
#3	Search micrococcus luteus reductase carbonyl	10:55:16	1
#2	Search micrococcus luteus reductase	10:55:07	36
#1	Search micrococcus luteus	10:55:00	1030

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#)

Jul 27 2004 13:14:01

BD141394
 LOCUS BD141394 834 bp DNA linear PAT 18-SEP-2002
 DEFINITION Novel carbonyl reductase, gene thereof and method of using the same.
 ACCESSION BD141394
 VERSION BD141394.1 GI:23236339
 KEYWORDS WO 0210399-A/1.
 SOURCE Micrococcus luteus
 ORGANISM Micrococcus luteus
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus.
 REFERENCE 1 (bases 1 to 834)
 AUTHORS Kizaki,N., Yasohara,Y. and Hasegawa,J.
 TITLE Novel carbonyl reductase, gene thereof and method of using the same
 JOURNAL Patent: WO 0210399-A 1 07-FEB-2002;
 KANEKA CORP,NORIYUKI KIZAKI,YOSHIHIKO YASOHARA,JUNZO HASEGAWA
 COMMENT OS Micrococcus luteus
 PN WO 0210399-A/1
 PD 07-FEB-2002
 PF 01-AUG-2001 WO 2001JP006619
 PR 01-AUG-2000 JP 00P 232756
 PI NORIYUKI KIZAKI,YOSHIHIKO YASOHARA,JUNZO HASEGAWA PC
 C12N15/53,C12N9/02,C12N1/21,C12P17/10// (C12N15/53,C12R1:265) CC
 Novel carbonyl reductase, gene thereof and method of using the same.
 CC same.
 FH Key Location/Qualifiers
 FT source 1..834
 FT /organism='Micrococcus luteus'.
 FEATURES Location/Qualifiers
 source 1..834
 /organism="Micrococcus luteus"
 /mol_type="genomic DNA"
 /db_xref="taxon:1270"

ORIGIN

Query Match 59.1%; Score 834; DB 6; Length 834;
 Best Local Similarity 100.0%; Pred. No. 5.8e-88;
 Matches 834; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	108	ATGCGACGGATGACGCTGCCGAGTGGGGAGTCCATCCCTGTGCTGGGCCAGGGCACCTGG	167
Db	1	ATGCGACGGATGACGCTGCCGAGTGGGGAGTCCATCCCTGTGCTGGGCCAGGGCACCTGG	60
Qy	168	GGCTGGGGTGAGGACCCGCGCCGCGGCGACGAGGTCGCCGCGCTGCACGCCGGCCTC	227
Db	61	GGCTGGGGTGAGGACCCGCGCCGCGGCGACGAGGTCGCCGCGCTGCACGCCGGCCTC	120
Qy	228	GAGCTGGGCATGACGCTGGTCGACACCGCCGAGATGTACGCCGACGGCGGTGCGGAGGAG	287
Db	121	GAGCTGGGCATGACGCTGGTCGACACCGCCGAGATGTACGCCGACGGCGGTGCGGAGGAG	180
Qy	288	GTGGCTGGTGAAGCATTGGCGGGTCGCCGCGACGAGGCGTTTCGTGGTCAGCAAGGTCATG	347
Db	181	GTGGCTGGTGAAGCATTGGCGGGTCGCCGCGACGAGGCGTTTCGTGGTCAGCAAGGTCATG	240

[illegible]

RESULT 2

ABU22187

ID ABU22187 standard; protein; 281 AA.

XX

AC ABU22187;

XX

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #7714.

XX

KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX

OS Burkholderia mallei.

XX

PN WO200277183-A2.

XX

PD 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX

PA (ELIT-) ELITRA PHARM INC.

XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

DR WPI; 2003-029926/02.

DR N-PSDB; ACA26057.

XX

PT New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

PS Claim 25; SEQ ID NO 50111; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 281 AA;

Query Match 55.4%; Score 806; DB 6; Length 281;
 Best Local Similarity 55.2%; Pred. No. 2e-69;
 Matches 153; Conservative 39; Mismatches 85; Indels 0; Gaps 0;

```

Qy      1 MRRMTLPAGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEE 60
      :  : || || : | |||| | | : | : || | : ||||| : |||| | |
Db      5 LETVALPGGERVPKLGQGTWEMGERPAKRAAEIAALREGVDLGMTLIDTAEMYGDGATET 64

Qy     61 VAGEALAGRDEAFVVSVMPSHASRSGTIAACERSLKRLGTDRLDLYLLHWQGRYPLQD 120
      : | : || | | : | : ||||| : |||| | : |||| | || : ||||| : || :
Db     65 LVGDALADVRLRFIVSKVLPHHASRGVVAACEATLKRLRTDRVDLYLLHWGRSIPLAIE 124

Qy    121 TVAAFHQLVEDGKIRYWGVSNFDHRLAELQDVPGTSGLTDDQVLYNLSRRGPEYDLLPW 180
      | : | | | : ||||| |||| | : | | : || : ||||| : ||||| : ||||
Db    125 TIAGFEALRDAGKIRYWGVSNFDVDDMEALVAEAGGAVCATDQILYNLARRGPEFDLLPW 184

Qy    181 CADHQLPVMAYSPIEQGRILDDTTLNDVAARHSVSPAAAALAWVLRRDSLCTIPKASSPQ 240
      | : : | : ||||| : | : | : || | ||||| : : : |||| | :
Db    185 LARREMPAIAYSPIDHMLPKRTALDEIARERGVSPTRVALAWVLGQPNVLAIPKAGSVE 244

Qy    241 HVRDNATALDVELTREDLDALDRAFPSPGPRPLEML 277
      |||| | || : | | : | | | | |||||
Db    245 HVRDNRAALDLVLGEEELARLDAQFKSPRGKRPLEML 281
  
```

RESULT 1

US-09-252-991A-29664

; Sequence 29664, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 29664

; LENGTH: 352

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29664

Query Match 55.8%; Score 812; DB 4; Length 352;

Best Local Similarity 56.8%; Pred. No. 4.6e-80;

Matches 158; Conservative 44; Mismatches 70; Indels 6; Gaps 4;

```

Qy      1 MRRMTLPSGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEE 60
      |: :| | |: : :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      80 MKTLTLIDGQEVAAIGQGTWHIGEQPGERKREVAALREGIELGMTLIDTAEMYAEGGAED 139

Qy      61 VAGEALAGRREAFVVSVMPSHASRSGTIAACERSLKRLGTDRIDL YLLHWQGRYPLQD 120
      | | |: | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      140 VVGAAIAGRREEVFLVSKVYPHNASRKGLPAACERSLRRLGCETIDL YLLHWQGRYPLEE 199

Qy      121 TVAAFHQLVEDGKIRYWGVS NFDHRALAE LQDVPGTSGLT TDQVLYNLSRRGP EYDLLPW 180
      |: | | :| : | | | | | | | | | | | | | | | | | | | | | | | |
Db      200 TIEAFERLRDQ GKILRWGVS NFD---LGD MYELDG-SACATNQVMYNLEERG IEYDLLPW 255

Qy      181 CADHQLPVMAYSPIEQ-GRILDDTTLNDVAARHSVSPAAAALAWVLRRDSLCTIPKASSP 239
      | : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      256 CQERGMPVMAYCPVGQGGRLLRHPALGEI AARHDASSAQVALAWLLEQ-GVIAIPKAVTS 314

Qy      240 QHVRDNATALDVELTREDLDALDRAFP PPSGPRPLEML 277
      |: | | | |: | | : | | | | | | | | | | | | | | | | |
Db      315 AHIRQNAAAADLELSADDLRLALDQAFPPPTRKRNLAIV 352

```

RESULT 2

US-09-489-039A-7896

; Sequence 7896, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 7896

; LENGTH: 324

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-7896

Query Match 47.2%; Score 686.5; DB 4; Length 324;
Best Local Similarity 48.9%; Pred. No. 2e-66;
Matches 139; Conservative 45; Mismatches 93; Indels 7; Gaps 3;

Qy 1 MRRMTLPSTGE--SIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGA 58
| : | : | | : : | : | | | | : | | | | | : : | : | : | | | | | | | |
Db 41 MVKKT VRFGEQA AVPAIGLGTWYMG EHA AQRQQEVAALRVGIDHGLTVIDTAEMYADGGA 100

Qy 59 EEVAGEALAGRRDEAFVSVKVMPSHASRSGTIAACERSLKRLGTDRIDL YLLHWQGRYPL 118
| | | | : : | : | | : | | | | | | | : : | | | | : : | | | | : | | |
Db 101 EEVVGQAIRGLRDRVVLVSKVYPWHAGKAAMHRACENSLRRLQTDYLDMYLLHWRGDIPL 160

Qy 119 QDTVA AFHQ LVEDGKIRYWGVS NFDHRA LAELQDVP GTSGLT TDQVLYNLSRRGPEYDLL 178
| : | | | : | | : | | | | | | | | : | | | | | : | | | | : | | | | |
Db 161 QETVEAMEKLVAEGKIRRWGVS NLDTEDMQALWRTADGEHCATNQVLYHLASRGIEYDLL 220

Qy 179 PWCADHQLPVMAYSPIEQ-GRILD----DTTLNDVAARHSVSPAAAAALAWVLRRDSLCTI 233
| | | | | | | | | : | | : | : : : : | : : | | | | : | : |
Db 221 PWCQQHSLPVMAYCPLAQAGRLRDGLFQHSDIINMANARGITVAQLLLAWVIRHPGVLAI 280

Qy 234 PKASSPQHVRDNATALDVELTREDLDALDRAFP PPSGPRPLEML 277
| | | : | : | | | | | : | : | | | : | | | : | : | : | : | : | : | : | :
Db 281 PKAASIEHV VQNA AALDIVLSGEEL AQLDRLYPPPQRKTRLD MV 324

RESULT 1

A97604

probable oxidoreductase (PA0804) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002

C;Accession: A97604

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, B.S.; Cao, Y.; Askenazi, M.; Halling, C.; Mullin, L.; Houmiel, K.; Gordon, J.; Vaudin, M.; Iartchouk, O.; Epp, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Flanagan, C.; Crowell, C.; Gurson, J.; Lomo, C.; Sear, C.; Strub, G.; Cielo, C.; Slater, S.

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58.

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: A97604

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-281 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK87786.1; PID:g15157157; GSPDB:GN00169

C;Genetics:

A;Gene: AGR_C_3682

A;Map position: circular chromosome

C;Superfamily: aldehyde reductase

Query Match 55.7%; Score 810; DB 2; Length 281;
Best Local Similarity 57.7%; Pred. No. 3.5e-62;
Matches 158; Conservative 35; Mismatches 81; Indels 0; Gaps 0;

Qy 4 MTLPSGESIPVLGQGTWGWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEVAG 63
:||||| :| || ||| || ||: :: :||||||| ||| :||| |
Db 8 VTLPSGNEVPALGLGTWNMGETRSSADDEIESIRKAIDLGMTLVDTAEMYADGRSEEVVG 67

Qy 64 EALAGRREAFVVSQVMPSHASRSGTIAACERSLKRGLTDRIDLKLLHWQGRYPLQDTVA 123
|:||||| |:||||| :|| || ||||| ||||| ||||| |:|| :|||
Db 68 TAIAGRREDEVFLVSKVPWNASARGTAEACERSLARLGTDHIDLKLLHWRGEHPLGETVA 127

Qy 124 AFHQLVEDGKIRYWGVSFNDHRALAEQDVPGTSGLTDDQVLYNLSRRGPEYDLLPWCAD 183
|| :| ||||| ||||| : || || :||||||| ||| : ||||| :
Db 128 AFERLKSQDGKIGNWGVSNFDTDDMEELFTVPEGKNCAANQVLYNLSRRGPEFSLLPWCQE 187

Qy 184 HQLPVMAYSPIEQGRILDDTTLDVAARHSVSPAAAALAWVLRRDSLCTIPKASSPQHVR 243
| :|:||||| ||||| : | :| : || |||:| || : |||:| :
Db 188 HGVPLMAYSPIEQGRILKNHELIRIAKAYQATPAQLALAFLLDRDGVIAIPKSASVSRIV 247

Qy 244 DNATALDVELTREDLDALDRAFPFPPSGPRPLEML 277
:| |||:| || ||| |||||: |||||
Db 248 ENRGATDLEITEEDWTALDAAFPPPTRKTSLEML 281

RESULT 2

AB2826

aldo/keto reductase Atu2032 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

C;Accession: AB2826

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Kitajima, J.P.; Okura, V.K.; Almeida Jr., N.F.; Zhou, Y.; Bovee Sr., D.; Chapman, P.; Clendenning, J.; Deatherage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutuyavin, T.; Levy, R.; Li, M.; McClelland, E.; Palmieri, A.; Raymond, C.; Rouse, G.; Saenphimmachak, C.; Wu, Z.; Gordon, D.; Eisen, J.A.; Paulsen, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B.; Liao, L.; Kim, S.; Hendrick, C.; Zhao, Z.; Dolan, M.; Tingey, S.V.; Tomb, J.; Gordon, M.P.; Olson, M.V.; Nester, E.W.

A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AB2826

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-281 <KUR>

A;Cross-references: GB:AE008688; PIDN:AAL43024.1; PID:g17740488; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu2032

A;Map position: circular chromosome

C;Superfamily: aldehyde reductase

Query Match 55.7%; Score 810; DB 2; Length 281;
Best Local Similarity 57.7%; Pred. No. 3.5e-62;
Matches 158; Conservative 35; Mismatches 81; Indels 0; Gaps 0;

```
Qy      4 MTLPSGESIPVLGQGTWCWGEDPGRRGDEVAALHAGLELGMTLVDTAEMYADGGAEVAG 63
      :| | | | | :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      8 VTLPSGNEVPALGLGTWNMGETRSSADDEIESIRKAIDLGMTLVDTAEMYADGRSEEVVG 67

Qy     64 EALAGRDEAFVVSVKVMPSHASRSGTIAACERSLKRGLGTDRIDL YLLHWQGRYPLQDTVA 123
      | :| | | | | | | | | | | :| | | | | | | | | | | | | | | | | | | | |
Db     68 TAIAGRDEVFLVSKVYPWNASARGTAEACERSLARLGTDHIDL YLLHWRGEHPLGETVA 127

Qy    124 AFHQLVEDGKIRYWGVS NFDHRAELQDVPGTSGLT TDQVLYNLSRRGPEYDLLPWCAD 183
      | | :| | | | | | | | | | | :| | | | | | | | | | | | | | | | | | | |
Db    128 AFERLKSDGKIGNWGVS NFDTDMEELFTVPEGKNCAANQVLYNLSRRGPEFSLLPWCQE 187

Qy    184 HQLPVMAYSPIEQGRILDDTTLNDAARHSVSPAAAALAWVLRRDSLCTIPKASSPQHVR 243
      | :| :| | | | | | | | | | | :| :| :| :| | | | | | | | | | | | | |
Db    188 HGVPLMAYSPIEQGRILKNHELIRIAKAYQATPAQLALAFLLDRDGVIAIPKSASVSRIV 247

Qy    244 DNATALDVELTREDLDALDRAFPSPGPRPLEML 277
      :| | | :| :| | | | | | | | | | | | | | | | | | | | | | | | | |
Db    248 ENRGATDLEITEEDWTALDAAFPPTRKTSLEML 281
```